

SUPPLEMENTARY DATA

APPENDIX S1

Alternative methods used for the maximum parsimony analyses

Searching for all of the islands of most-parsimonious trees is an important step in any analysis that uses parsimony as the optimal criterion (Maddison, 1991; Page, 1993), but the time necessary to conduct such tree-space's explorations increases logarithmically with the size of the data matrix (Nixon, 1999). If the trees found with the branch swapping algorithm are all kept and swapped themselves, the search often aborts because the computer runs out of memory. In order to avoid this problem and to limit the number of trees swapped during each replicate while maximizing exploration of the tree-space for islands of equally parsimonious trees, two independent methods were used for the analysis of the *psbA-trnH*, *trnQ-rps16*, *nad1-2/3*, *nad4-1/2* and ITS regions and for the combined dataset. First, heuristic searches were modified to keep only the 500 first most parsimonious trees of each replication (nchuck = 500 chucksize = 1). Second, parsimony ratchet (Nixon, 1999) searches consisting of 20 independent replicates of 200 iterations with 15% of characters reweighted per iteration were scripted using the program PAUPRat (Sikes and Lewis, 2001) and run in the program PAUP*. In both cases, strict and majority-rule consensus trees were calculated from all most parsimonious trees and the robustness of nodes was evaluated using MP with 1000 bootstrap replicates of new heuristic searches (100 random addition replicates, TBR branch swapping, multrees off).

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APPENDIX S2

Method used to define geographical areas as character states to infer the ancestral patterns of distribution

Species were grouped firstly in accordance with the two major centres of diversity already identified for the genus *Sisyrinchium* (Cocucci and Vogel, 2001): area A was defined along the subandean ranges, between Chile and Argentina, and area B was delimited around the Paraná river basin. The remaining species were divided into two major areas, according to morphological similarities shown by most of the species included in these geographical subdivisions. The vast majority of the *Sisyrinchium* species described between the south-western part of the United States and Bolivia (area C) are included in the subgenus *Echtronema* and are morphologically closely related (Klatt, 1861; Baker, 1892; Bicknell, 1900; Macbride, 1936; Rudall *et al.*, 1986; Henrich and Goldblatt, 1987, Calderón de Rzedowski, 1988; McVaugh, 1989; Goldblatt *et al.*, 1990; Espejo-Serna and López-Ferrari, 1996; Cholewa and Henderson, 2002; Barker, 2004), even if morphological, anatomical and cytological discordances emerge in this subdivision. Area D was delimited in order to cover the distribution area of North American species gathered in the subgenus *Sisyrinchium* (Goldblatt *et al.*, 1990) and represents the vast majority of the *Sisyrinchium* species distributed in the area thus defined. These species exhibit a strongly homogeneous morphological pattern and they are often not easily distinguished from each other apparently because of

the phenotypic plasticity within species which conduct the discriminatory morphological characters to overlap (Cholewa and Henderson, 2002). Almost all of them bear few stipitate glandular trichomes on the lower half-part of the filamental column and, although their secretion content is still unknown, no oil-collecting bees have been recorded to pollinate or visit *Sisyrinchium* species in that area (Cocucci and Vogel, 2001). This body of evidence features a well-discriminated group of species.

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